SEQUENCE LISTING

(1)   GENERAL INFORMATION:

(i)   APPLICANT: Li, ET AL.

(ii)   TITLE OF INVENTION: Human G-Protein Chemokine Receptor

(iii)   NUMBER OF SEQUENCES:

(iv)   CORRESPONDENCE ADDRESS:

     (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
     (B) STREET: 6 BECKER FARM ROAD
     (C) CITY: ROSELAND
     (D) STATE: NEW JERSEY
     (E) COUNTRY: USA
     (F) ZIP: 07068

(v)   COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: 3.5 INCH DISKETTE
     (B) COMPUTER: IBM PS/2
     (C) OPERATING SYSTEM: MS-DOS
     (D) SOFTWARE: WORD PERFECT 5.1

(vi)   CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER:
     (B) FILING DATE: concurrently
     (C) CLASSIFICATION:

(vii)   ATTORNEY/AGENT INFORMATION:
     (A) NAME: FERRARO, GREGORY D.
     (B) REGISTRATION NUMBER: 36,134
     (C) REFERENCE/DOCKET NUMBER: 325800-

(viii) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: 201-994-1700
     (B) TELEFAX: 201-994-1744

(2)   INFORMATION FOR SEQ ID NO:1:

(i)   SEQUENCE CHARACTERISTICS
     (A) LENGTH: 1414 BASE PAIRS
     (B) TYPE: NUCLEIC ACID
     (C) STRANDEDNESS: SINGLE
     (D) TOPOLOGY: LINEAR

(ii)   MOLECULE TYPE: cDNA

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GTGAGATGGT GCTTTCATGA ATTCCCCCAA CAAGAGCCAA GCTCTCCATC TAGTGGACAG    60
```

GGAAGCTAGC AGCAAACTTT CCCTTCACTA CGAAACTTCA TTGCTTGGCC CAAAAGAGAG 120

TTAATTCAAT GTAGACATCT ATGTAGGCAA TTAAAAACCT ATTGATGTAT AAAACAGTTT 180

GCATTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTTATTTA 240

TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291
                 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp

ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339
Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln

ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387
Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe

GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435
Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln

AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483
Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser

GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531
Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala

GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579
Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly Leu Tyr

TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627
Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln Leu Leu Thr

ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675
Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala

AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG 723
Arg Thr VaL Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val

GCT GTG TTT GCG TCT CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA 771
Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys

GAA GGT CTT CAT TAC ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT 819
Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr

CAA TTC TGG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG 867
Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu

GTC CTG CCG CTG CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA 915
Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys

ACT CTG CTT CGG TGT CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG 963
Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg

CTT ATC TTC ACC ATC ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC 1011
Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr

AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT 1059
Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn

AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG 1107
Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu

ACT CTT GGG ATG ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT 1155
Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe

-45-

```
GTC GGG GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC    1203
Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His

ATT GCC AAA CGC TTC TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT    1251
Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala

CCC GAG CGA GCA AGC TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA    1299
Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu

ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG    1354
Ile Ser Val Gly Leu

TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCTTTT   1414
```

(2)   INFORMATION FOR SEQ ID NO:2:
   (i) SEQUENCE CHARACTERISTICS
        (A) LENGTH: AMINO ACIDS
        (B) TYPE: AMINO ACID
        (C) STRANDEDNESS:
        (D) TOPOLOGY: LINEAR

   (ii)   MOLECULE TYPE: PROTEIN

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr
                      5                  10                 15
Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala
                     20                  25                 30
Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe
                     35                  40                 45
Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg
                     50                  55                 60
Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
                     65                  70                 75
Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala
                     80                  85                 90
Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly
                     95                 100                105
Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln
                    110                 115                120
Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
                    125                 130                135
Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val
                    140                 145                150
Ile Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile
                    155                 160                165
Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser
                    170                 175                180
His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr
                    185                 190                195
Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val Met
                    200                 205                210
```

-46-

Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg
215   220   225

Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
230   235   240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu
245   250   255

Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser
260   265   270

Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu
275   280   285

Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val
290   295   300

Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His
305   310   315

Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu
320   325   330

Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
335   340   345

Gln Glu Ile Ser Val Gly Leu
350